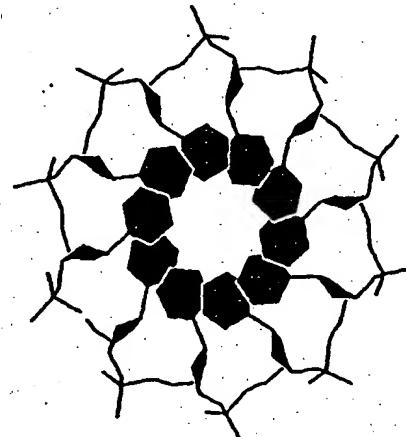


Appendix A

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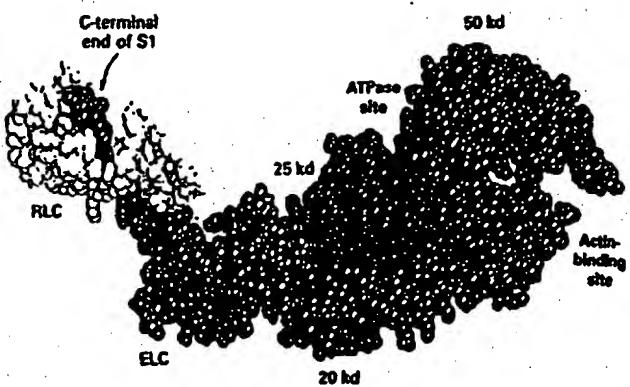
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Figure 15-11
 Three-dimensional structure of the S1 head of myosin determined by x-ray crystallography at 2.8 Å resolution. The nucleotide-binding site is empty in this crystal form. The heavy chain of S1 consists of a 25-kd N-terminal domain (purple), a 50-kd central domain (blue), and a 20-kd C-terminal domain (red). The actin-binding site and the ATPase site are on opposite sides of the 50-kd domain. Two light chains (RLC, yellow, and ELC, green) are bound to the long C-terminal α helix of the heavy chain. [Courtesy of Dr. Ivan Rayment and Dr. Hazel Holden.]



ments, whereas the actin-binding site is formed by the 50-kd and 20-kd segments. Nearly all known myosins share the catalytic-site sequence



which is similar to the sequences found in the active sites of other ATPases. The two light chains wrap around the 20-kd segment, which forms an 85-Å-long α helix that spans much of S1.

The two S1 heads are joined at a hinge to the tail of myosin, which is a two-stranded coiled coil (Figure 15-12). The formation of this very long rod (1700 Å, or 170 nm) is favored by the absence of proline over a span of more than a thousand residues and by the abundance of leucine, alanine, and glutamate. The two strands are in register, pointing the same way. Their axes are about 10 Å apart, enabling the side chains of the two strands to interact intimately to reinforce the helical structure. Regularities in the amino acid sequence of the tail promote the formation of a coiled-coil rod. The tail consists of repeating seven-residue units (abcdefg) in which *a* and *d* are usually hydrophobic (Figure 15-13). Residues *a* and *d* form a zigzag pattern of knobs and holes that interlock with those of the other strand to form a tight-fitting hydrophobic core. In contrast, residues *b*, *c*, and *f*, which are located on the periphery of the coiled coil, tend to be charged.

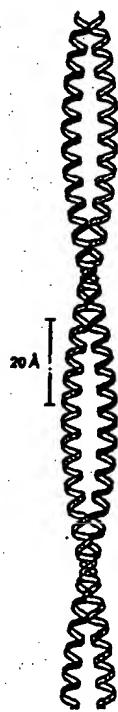


Figure 15-12
 Model of a two-stranded α -helical coiled coil.

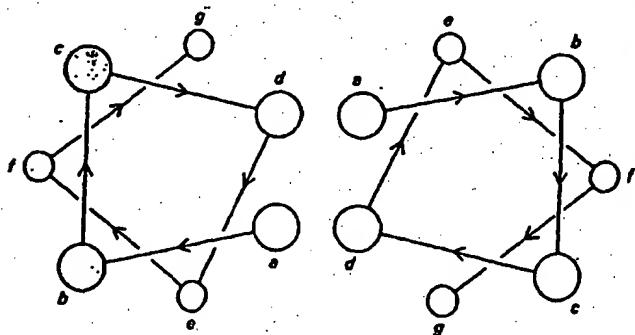


Figure 15-13
 Schematic diagram of a cross section of an α -helical coiled coil showing the positions of side chains. Residues *a* and *d* (yellow) of each strand pack tightly to form a hydrophobic core. Residues *b*, *c*, and *f* (green) on the periphery tend to be charged.